

FIG. 1

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LINKER #1 15bp | SV40 ORIGIN=332bp
 GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCACTGGGGC 120
 GGAGAATGGG CGGAACCTGGG CGGAGTTAGG GGCAGGGATGG GCGGAGTTAG GGGCGGGACT 180
 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCACTACTTC TGCCCTGCTGG GGAGCCTGGG 240
 GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
 GGGGAGCCTG GGGACTTTCC ACACCCCTAAC TGACACACAT TCCACAGAAAT TAATTCCCCCT |
 347 8 360 1 LINKER #2=13bp
 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATAT GCCCATATAT GGAGTTCCGC 420
 GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
 CMV PROMOTER-ENHANCER=567bp
 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
 TGGGTGGACT ATTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTATC TCAATATGCCA 600
 AGTACGCCAC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTAT TGCCCACTAC 660
 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
 ATGGTGATGC GGTTTGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGGA 780
 TTTCCAAGTC TCCACCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG 840
 GACTTTCCAA AATGTCGTA CAACCTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTAA 900
 LINKER #3=76bp
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG 727 8 TACGTGAACC GTCAAGATCGC CTGGAGACGC 960
 Bgl II LEADER=60bp
 CATCACAGAT CTCTCACCAT 978 9 GAGGGTCCCC GCTCAGCTCC TGGGGCTCCT GCTGCTCTGG 1020
 +1 101 102 107 108
 CTCCCAGGTG CACGATGTGA TGGTACCAAG GTGGAAATCA AACGTACGGT GGCTGCACCA 1080
 1038 9 1062 3 Bsi WI
 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG 1140
 TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAAGGT GGATAACGCC 1200
 HUMAN KAPPA CONSTANT 324bp 107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAATCTCCA GGAGAGTGTAC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
 AGCCTCAGCA GCACCCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1320
 TGCAGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1380
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=85bp
 TGTGAATTCA AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTGT GACAACATGC 1440
 1386 7
 GGCCGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1500
 1471 2

FIG. 2A

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GTTTGCCCT CCCCCGTGCC TTCCCTGACC CTGGAAGGTG CCACCTCCAC TGTCCCTTCC 1560
 BGH poly A=231bp
 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1620
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1680
 | LINKER #5=15bp |
 GCGGTGGGCT CTATGGAACC AGCTGGGCT CGACAGCTAT GCCAAGTACG CCCCCATTG 1740
 1702 3 1717 8
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCA GTACATGACC TTATGGACT 1800
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTT 1860
 CMV PROMOTER-ENHANCER=334bp
 GGCAGTACAT CAATGGCGT GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC 1920
 CCATTGACGT CAATGGGAGT TTGTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 1980
 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
 | LINKER #6=7bp |
 TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100
 2051 2 2058 9
 | LEADER=51bp | Sal I 2151 | Mlu I 2 Nhe I
ATGGGTTGGA GCCTCATCTT GCTCTCCCTT GTCGCTGTTG CTACGCGTGT CGCTAGCACC 2160
 START HEAVY CHAIN -5 -4 -3 114 115
 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACACCG 2220
 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA 2280
 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
 HUMAN GAMMA 1 CONSTANT
 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 2400
 993bp=330 AMINO ACID & STOP CODON
 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGCAGAGCC CAAATCTTGT 2460
 GACAAAACTC ACACATGCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 2520
 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 2580
 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 2640
 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 2700
 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGACTACAAG 2760
 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 2820
 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAGG 2880
 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 2940
 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 3000

FIG. 2B

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GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 3060
 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 3120
 STOP HEAVY CHAIN Bam HI LINKER #7=81bp
 CTCTCCCTGT CTCCGGGTAA ~~AATGAGGATCC~~ GTTAACGGTT ACCAACTACC TAGACTGGAT 3180
 3144 5
 TCGTGACAAC ATGCGGCCGT GATATCTACG TATGATCAGC ~~CTCGACTGTG~~ CCTTCTAGTT 3240
 3225 6
 GCCAGCCATC TGTTGTTGC CCCTCCCCG TGCTTCCTT GACCCCTGGAA GGTGCCACTC 3300
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 CCACTGTCCT TTCTTAATAA AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT 3360
 CTATTCTGGG GGGTGGGGTG GGGCAGGACA GCAAGGGGAA GGATTGGGAA GACAATAGCA 3420
 LINKER #8=34bp
 GGCGATGCTGG GGATGCGGTG GGCTCTATGG AACCAAGCTGG GGCTCGACAG CGCTGGATCT 3480
 3456 7
 CCCGATCCCC AGCTTGCTT CTCAATTCT TATTGCATA ATGAGAAAAA AAGGAAAATT 3540
 3490 1
 AATTTAACCA CCAATTCACT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 3600
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 3660
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 3720
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 3780
 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTGCTT 3840
 LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
 CTGACATAGT TGTTGGGA GCTTGGATAG CTTGGACAGC TCAGGGCTGC GATTTCGGC 3900
 3856 7 3875 6 START DHFR
 CAAACTTGAC GGCAATCCTA GCGTGAAGGC TGGTAGGATT TTATCCCCGC TGCCATC 3960
 3957 8
 GTTCGACCAT TGAAC TGCACT CGTCGCCGTG TCCC AAAATA TGGGGATTGG CAAGAACGGA 4020
 GACCTACCCCT GGCCCTCCGCT CAGGAACGAG TTCAAGTACT TCCAAAGAAT GACCACAAACC 4080
 TCTTCAGTGG AAGGTAAACA GAATCTGGTG ATTATGGTA GGAAAACCTG GTTCTCCATT 4140
 MOUSE DHFR=564bp=187 AMINO ACID & STOP CODON
 CCTGAGAAGA ATCGACCTTT AAAGGACAGA ATTAATATAG TTCTCAGTAG AGAACTCAAA 4200
 GAACCACCAAC GAGGAGCTCA TTTTCTTGCC AAAAGTTGG ATGATGCCTT AAGACTTATT 4260
 GAACAAACCGG AATTGGCAAG TAAAGTAGAC ATGGTTTGG TAGTCGGAGG CAGTTCTGTT 4320
 TACCAAGGAAG CCATGAATCA ACCAGGCCAC CTTAGACTCT TTGTGACAAG GATCATGCAG 4380
 GAATTTGAAA GTGACACGTT TTTCCCAGAA ATTGATTGG GGAAATATAA ACTTCTCCCA 4440
 GAATAACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTGAA 4500

FIG. 2C

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STOP DHFR
 GTCTACGAGA AGAAAGAC~~TA~~ ACAGGAAGAT GCTTCAGT TCTCTGCTCC CCTCCTAAAG 4560
 4521 2

3' UNTRANSLATED DHFR=82bp LINKER #10=10bp
 TCATGCATTT TTATAAGACC ATGGGACTTT TGCTGGCTT AGATCAGCCT CGACTGTGCC 4620
 4603 4 4613 4

TTCTAGTTGC CAGCCATCTG TTGTTGCCC CTCCCCGTG CCTTCCTTGA CCCTGGAAGG 4680
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 TGCCACTCCC ACTGTCTTT CCTAATAAAA TGAGGAAATT GCATCGCATT GTCTGAGTAG 4740

GTGTCATTCT ATTCTGGGG GTGGGGTGGG GCAGGACAGC AAGGGGGAGG ATTGGGAAGA 4800
 CAATAGCAGG CATGCTGGGG ATGCGGTGGG CTCTATGGAA CCAGCTGGGG CTCGAGCTAC 4860
 4844 5

AGCTTTGCT TCTCAATTTC TTATTGCAT AATGAGAAAA AAAGGAAAAT TAATTTAAC 4920

ACCAATTCAAG TAGTTGATTG AGCAAATGCG TTGCCAAAAA GGATGCTTA GAGACAGTGT 4980
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 TCTCTGCACA GATAAGGACA AACATTATTC AGAGGGAGTA CCCAGAGCTG AGACTCCTAA 5040

GCCAGTGAGT GGCACAGCAT TCTAGGGAGA AATATGCTTG TCATCACCGA AGCCTGATT 5100

CGTAGAGCCA CACCTTGGTA AGGGCCAATC TGCTCACACA GGATAGAGAG GGCAGGAGCC 5160

AGGGCAGAGC ATATAAGGTG AGGTAGGATC AGTTGCTCCT CACATTGCT TCTGACATAG 5220

TTGTGTTGGG LINKER #12=21bp AGCTTGGATC GATCCTCTAT START NEO
 5227 8 5248 9 GTTGAACAA GATGGATTGC ACGCAGGTT 5280

TCCGGCCGCT TGGGTGGAGA GGCTATTGG CTATGACTGG GCACAAACAGA CAATCGGCTG 5340

CTCTGATGCC GCCGTGTTCC GGCTGTCAGC GCAGGGGCGC CCGGTTCTTT TTGTCAAGAC 5400
 NEOMYCIN PHOSPHOTRANSFERASE
 CGACCTGTCC GGTGCCCTGA ATGAACTGCA GGACGAGGCA GCGCGGCTAT CGTGGCTGGC 5460

795bp=264 AMINO ACIDS & STOP CODON
 CACGACGGGC GTTCCTTGCG CAGCTGTGCT CGACGTTGTC ACTGAAGCGG GAAGGGACTG 5520

GCTGCTATTG GGCGAAGTGC CGGGGCAGGA TCTCCTGTCA TCTCACCTG CTCCCTGCCG 5580

GAAAGTATCC ATCATGGCTG ATGCAATGCG GCGGCTGCAT ACGCTTGATC CGGCTACCTG 5640

CCCATTGAC CACCAAGCGA AACATCGCAT CGAGCGAGCA CGTACTCGGA TGGAAGCCGG 5700

TCTTGTGAT CAGGATGATC TGGACGAAGA GCATCAGGGG CTCGCGCCAG CCGAACTGTT 5760

CGCCAGGCTC AAGGCGCGCA TGCCCCACGG CGAGGATCTC GTCGTGACCC ATGGCGATGC 5820

CTGCTTGCCTG AATATCATGG TGGAAAATGG CCGCTTTCT GGATTGATCG ACTGTGGCCG 5880

GCTGGGTGTG GCGGACCGCT ATCAGGACAT AGCGTTGGCT ACCCGTGATA TTGCTGAAGA 5940

GCTTGGCGGGC GAATGGGCTG ACCGCTTCCT CGTGCTTAC GGTATCGCCG CTTCCCGATTG 6000

FIG. 2D

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STOP NEO
 GCAGCGCATC GCCTTCTATC GCCTTCTTGA CGAGTTCTTC ~~TGAG~~ GCGGGAC TCTGGGGTTC 6060
 604314

GAAATGACCG ACCAAGCGAC GCCCAACCTG CCATCACGAG ATTCGATT CACCGCCGCC 6120

3' UNTRANSLATED NEO=173bp
 TTCTATGAAA GGTTGGGCTT CGGAATCGTT TTCCGGGACG CGGGCTGGAT GATCCTCCAG 6180

CGCGGGGATC TCATGCTGGA GTTCTCGCC CACCCCAACT TGTTTATTGC AGCTTATAAT 6240
 6216 7

GGTTACAAAT AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTC TTCACTGCAT 6300

SV40 POLY A EARLY=133bp LINKER #13=19bp
 TCTAGTTGTG GTTTGTCAA ACTCATCAAT CTATCTTATC ATGTCGGAT CGCGGCCGCG 6360
 6349 50

ATCCCGTGA GAGCTTGGCG TAATCATGGT CATACTGTT TCCTGTGTGA AATTGTTATC 6420
 6368 9

CGCTCACAAT TCCACACAAAC ATACGAGCCG GAAGCATAAA GTGTAAGCC TGGGGTGCCT 6480

AATGAGTGAG CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCGCTTTC CAGTCGGAA 6540

ACCTGTGCGTGC CCAGCTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCCTA 6600

PVC 19
 TTGGGCGCTC TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC 6660

GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG 6720

CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT 6780

6792=BACTERIAL ORIGIN OF REPLICATION
 TGCTGGCGTT TCTCCATAGG CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA 6840

GTCAGAGGTG GCGAAACCCG ACAGGACTAT AAAGATAACCA GGCCTTTCCC CCTGGAAGCT 6900

CCCTCGTGCCT CTCTCCTGTT CCGACCCCTGC CGCTTACCGG ATACCTGTCC GCCTTCTCC 6960

CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020

TCGTTCGCTC CAAGCTGGC TGTGTGCACG AACCCCCCGT TCAGCCCGAC CGCTGCGCCT 7080

TATCCGGTAA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG 7140

CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA 7200

AGTGGTGGCC TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA 7260

AGCCAGTTAC CTTCGGAAAA AGAGTTGGTA GCTCTGATC CGGCAAACAA ACCACCGCTG 7320

GTAGCGGTGG TTTTTTGTT TGCAAGCAGC AGATTACCGCG CAGAAAAAAA GGATCTCAAG 7380

AAGATCCTT GATCTTTCT ACGGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTTAAG 7440

GGATTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTA AATTAAAAAT 7500

FIG. 2E

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STOP BETA LACTAMASE
GAAGTTTAA ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT 7560
7550
TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTCG TTCATCCATA GTTGCCGTGAC 7620
TCCCCGTCGT GTAGATAACT ACGATAACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA 7680
TGATACCGCG AGACCCACGC TCACCGGCTC CAGATTATC AGCAATAAAC CAGCCAGCCG 7740
BETA LACTAMASE=861bp
GAAGGGCCGA CGCGAGAAGT GGTCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT 7800
286 AMINO ACID & STOP CODON
GTTGCCGGGA AGCTAGAGTA AGTAGTTCGC CAGTTAATAG TTTGCGCAAC GTTGTGCCA 7860
TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTGGTAT GGCTTCATTG AGCTCCGGTT 7920
CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAAGCG GTTAGCTCCT 7980
TCGGTCCTCC GATCGTTGTC AGAAGTAAGT TGGCCGCAGT GTTATCACTC ATGGTTATGG 8040
CAGCACTGCA TAATTCTCTT ACTGTCATGC CATCCGTAAG ATGCTTTCT GTGACTGGTG 8100
AGTACTCAAC CAAGTCATTG TGAGAATAGT GTATGCCGCG ACCGAGTTGC TCTTGCCCGG 8160
CGTCAATAACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC ATCATTGGAA 8220
AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT GTTGAGATCC AGTTCGATGT 8280
AACCCACTCG TGACCCCAAC TGATCTTCAG CATCTTTAC TTTCACCAGC GTTTCTGGGT 8340
GAGCAAAAAC AGGAAGGCAA AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT 8400
START BETA LACTAMASE
GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
8410
TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACAA AATAGGGGTT CCGCGCACAT 8520
TTCCCCGAAA AGTGCCACCT

FIG. 2F

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LINKER #1=15bp
 GACGTCGCGG CCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
 15 6

AGGCCGAGGC GGCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
 SV40 ORIGIN=332bp
 GGAGAATGGG CGGAACTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180

ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTGCTGG GGAGCCTGGG 240

GACTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300

GGGGAGCCTG GGGACTTCC ACACCTAAC TGACACACAT TCCACAGAAAT TAATTCCCCT 360
 347 8
 LINKER #2=13bp

AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCAT A GCCATATAT GGAGTTCCGC 420

GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480

ACGTCAATAA TGACGTATGT TCCCAGTAGTA ACGCCAATAG GGACTTCCA TTGACGTCAA 540

CVM PROMOTER-ENHANCER=567bp
 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGT A TCATATGCCA 600

AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT A TGCCCAGTAC 660

ATGACCTTAT GGGACTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720

ATGGTGATGC GGTTTGCA GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGG 780

TTTCCAAGTC TCCACCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG 840

GACTTCCAA AATGTCGTA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGT 900

LINKER #3=7bp
 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
 927 8 934 5

Bgl 2 START LIGHT CHAIN NATURAL LEADER=66bp
 CATCACAGAT CTCTCACTAT GGATTTCAAG GTGCAGATT A TCAGCTTCCCT GCTAATCACT 1020
 978 9

GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
 1044 5⁺¹

GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAAGGCCA GCTGAAGTGT AAGTTACATC 1140

CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCCT GGATTTATGC CACATCCAAC 1200

LIGHT CHAIN VARIABLE REGION 318bp 106 AMINO ACID
 CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTACTCTCTC 1260

ACCATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320

AACCCACCCA CGTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
 1362 3

TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAACTGC CTCTGTTGTG 1440

TGCCTGCTGA ATAACCTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAGGT GGATAACGCC 1500

FIG. 3A

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HUMAN KAPPA CONSTANT=324bp=107 AMINO ACID & STOP CODON
 CTCCAATCGG GTAACTCCCA GGAGAGTGT~~C~~ ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1560
 AGCCTCAGCA GCACCCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA AGTCTACGCC 1620
 TGCAGAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA AGAGCTTCAA CAGGGGAGAG 1680
 STOP
 LIGHT
 CHAIN Eco RI LINKER #4=81bp
 TGT~~T~~GAATT~~C~~ AGATCCGTTA ACGGTTACCA ACTAC~~C~~TAGA CTGGATT~~C~~GT GACAACAT~~G~~C 1740
 1646~~7~~ 1771~~2~~ |
 GGCGGTGATA TCTACGTATG ATCAGCCTCG ACTGTGCCTT CTAGTTGCCA GCCATCTGTT 1800
 GTTTGCCTCT CCCCGTGCCT TTCCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCCTTCC 1860
 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGGGTGGGGC AGGACAGCAA GGGGGAGGAT TGGGAAGACA ATAGCAGGCA TGCTGGGGAT 1980
 LINKER #5=15bp
 GCGGTGGGCT CTATGGAACC AGCTGGGCT CGACAGCTAT GCCAAGTACG CCCCCTATTG 2040
 2002~~3~~ 2017~~8~~ |
 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCA GTACATGACC TTATGGGACT 2100
 TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTT 2160
 CMV PROMOTER-ENHANCER=334bp
 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTCCA AGTCTCCACC 2220
 CCATTGACGT CAATGGGAGT TTGTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC 2280
 GTAACAACTC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2340
 LINKER #6=7bp Sal I
 TAAGCAGAGC TGGGTACGT~~C~~ CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2400
 START 2351~~2~~ 2358~~9~~ |
 HEAVY CHAIN SYNTHETIC & NATURAL LEADER Mlu I 2457~~18~~
 ATGGGTTGGA GCCTCATCTT GCTCTCCTT GTCGCTGTTG CTACGGTGT~~C~~ CCTGTC~~C~~CAG 2460
 2401 -5 -4 -3 -2 -1 +1 |
 GTACAAC~~T~~GC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTAGT GAAGATGTCC 2520
 TGCAAGGCTT CTGGCTACAC ATTTACCA~~G~~T TACAATATGC ACTGGGTAAA ACAGACACCT 2580
 HEAVY CHAIN VARIABLE=363bp=121 AMINO ACID
 GGT~~CGGGGCC~~ TGGAA~~TGG~~AT TGGAGCTATT TATCCCGGAA ATGGT~~G~~ATAC TTCCTACAAT 2640
 CAGAAGTTCA AAGGCAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG 2700
 CAGCTCAGCA GCCTGACATC TGAGGACTCT GCGGTCTATT ACTGTGCAAG ATCGACTTAC 2760
 TACGGCGGTG ACTGGTACTT CAATGTCTGG GGCGCAGGGA CCACGGTCAC CGTCTCTGCA 2820
Nhe I
 GCTAGCACCA AGGGCCC~~A~~TC GGTCTTCCCC CTGGCACCC~~T~~ CCTCCAAGAG CACCTCTGGG 2880
 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGT~~C~~G 2940
 HUMAN GAMMA 1 CONSTANT=993bp
 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGT~~C~~C~~T~~ ACAGTCCTCA 3000

FIG. 3B

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330 AMINO ACID & STOP CODON
 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 3060
 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGCAGAGCCC 3120
 AAATCTTGTG ACAAAAATCA CACATGCCA CCGTGCCCCAG CACCTGAAC TCTGGGGGGA 3180
 CCGTCAGTCT TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT 3240
 GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
 TACGTGGACG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC 3360
 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
 GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC 3480
 AAAGCCAAAG GGCAGCCCCG AGAACACACAG GTGTACACCC TGCCCCCATC CCGGGATGAG 3540
 CTGACCAAGA ACCAGGTCAAG CCTGACCTGC CTGGTCAAAG GCTTCTATCC CAGCGACATC 3600
 GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT ACAAGACCAC GCCTCCCGTG 3660
 CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA CCGTGGACAA GAGCAGGTGG 3720
 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
 STOP HEAVY CHAIN ^{Bam HI} LINKER #7=81bp
 CAGAAGAGCC TCTCCCTGTC TCCGGGTAA [TGAGGGATCCG TTAACGGTTA CCAACTACCT 3840
 3813 4
 AGACTGGATT CGTGACAACA TGCAGGCCGTG ATATCTACGT ATGATCAGCC TCGACTGTGC 3900
 3894 5
 CTTCTAGTTG CCAGCCATCT GTTGTGTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAAG 3960
 GTGCCACTCC CACTGTCCCTT TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA 4020
 BOVINE GROWTH HORMONE POLYADENYLATION REGION=231bp
 GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080
 ACAATAGCAG GCATGCTGGG GATGCGGTGG GCTCTATGGA ACCAGCTGGG GCTCGACAGC 4140
 4125 6
 GCTGGATCTC CCGATCCCCA GCTTTGCTTC TCAATTCTT ATTTCGATAA TGAGAAAAAA 4200
 AGGAAAATTA ATTTAACAC CAATTCAAGTA GTTGATTGAG CAAATGCGTT GCCAAAAAGG 4260
 MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 ATGCTTACA GACAGTGGTC TCTGCACAGA TAAGGACAAA CATTATTCAAG AGGGAGTACC 4320
 CAGAGCTGAG ACTCCTAACG CAGTGAGTGG CACAGCATTG TAGGGAGAAA TATGCTTGTC 4380
 ATCACCGAAG CCTGATTCCG TAGAGCCACA CCTTGGTAAG GGCACATCTG CTCACACAGG 4440
 ATAGAGAGGG CAGGAGCCAG GGCAGAGCAT ATAAGGTGAG GTAGGATCAG TTGCTCCTC 4500

FIG. 3C

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CATTTGCTTC TGACATAGTT LINKER #9=19bp 5' UNTRANSLATED DHFR=82bp
 4525 6 4544 5 4560

ATTTCGCGCC AAACTTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATT TATCCCCGCT 4620

START DHFR
 GCCATC~~ATGG~~ TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
 4626 7

AAGAACGGAG ACCTACCCCTG GCCTCCGCTC AGGAACGGAGT TCAAGTACTT CCAAAGAATT 4740

ACCACAAACCT CTTCA~~GT~~AGTGG~~A~~ AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800

DHFR=564bp=187 AMINO ACID & STOP CODON
 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCA~~G~~TAGA 4860

GAAC~~T~~CAAAG AACCA~~CC~~ACACG AGGAGCTCAT TTTCTTGCCA AAAGTTGG~~A~~ TGATGCC~~T~~TA 4920

AGACTTATTG AACAA~~CC~~GGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980

AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040

ATCATGCAGG AATTGAAAG TGACACGTTT TTCCCAGAAA TTGATTGG~~G~~ GAAATATAAA 5100

CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAA~~G~~ CATCAAGTAT 5160

STOP DHFR 3' UNTRANSLATED DHFR=82bp
 AAGTTTGAAG TCTACGAGAA GAAAGAC~~TAA~~ CAGGAAGATG CTTCAAGTT CTCTGCTCCC 5220
 5140 1

LINKER #10
 CTCC~~T~~AAAGC TATGCATTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC 5280
 5272 3
=10bp
 GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGC~~CC~~ TCCCCCGTGC CTTCC~~T~~TGAC 5340

BOVINE GROWTH HORMONE POLYADENYLATION=231bp
 CCTGGAAGGT GCCACTCCC~~A~~ CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCAT~~TG~~ 5400

TCTGAGTAGG TGT~~C~~ATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460

LINKER #11
 TTGGGAAGAC AATAGCAGGC ATGCTGGGA TGCGGTGGGC TCTATGGAAC CAGCTGGGGC 5520
 5513 4

=17bp
 TCGAGCTACT AGCTTTGCTT CTCAATTCT TATTTC~~G~~ATA ATGAGAAAAA AAGGAAAATT 5580
 5530 1

AATTTTAACA CCAATTCA~~G~~ AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640

MOUSE BETA GLOBIN MAJOR PROMOTER=366bp
 AGACAGTGTT CTCTGCACAG ATAAGGACAA CTAGGGAGAA ATATGCTTGT CATCACCGAA 5700

GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760

GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820

GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880

LINKER #12=21bp START NEO
 CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCCTCT~~TATG~~ GTTGAACAAG ATGGATTGCA 5940
 5896 7 5917 8

CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTGCC TATGACTGGG CACAAACAGAC 6000

FIG. 3D

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AATCGGCTGC TCTGATGCCG CCGTGTCCG GCTGTCAGCG CAGGGGCGGC CGGTTCTTT 6060
 NEOMYCIN PHOSPHOTRANSFERASE=795bp=264 AMINO ACID & STOP CODON
 TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAACGTGAG GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGCAG AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGGACTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCGTGATC CTCACCTTGC 6240
 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCCG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTGACCC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 GGAAGCCGGT CTTGTCGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTG GCCAGGCTCA AGGCGCGCAT GCCCCGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTCTG GATTGATCGA 6540
 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATTAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTAUG GTATCGCGC 6660
 STOP NEO
 TCCCGATTG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTC~~G~~ GAGCGGGACT 6720
 6712 3
 CTGGGGTTCG AAATGACCGA CCAAGCGACG CCCAACCTGC CATCACGAGA TTTCGATTCC 6780
 3' UNTRANSLATED NEO=173bp
 ACCGGCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTT TCCGGGACGC CGGCTGGATG 6840
 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTGCCG ACCCGAACCTT GTTATTGCA 6900
 6885 6
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTT 6960
 SV40 EARLY POLYADENYLATION REGION=133bp
 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
 7018 9
 LINKER #13=19bp
 GCGGCCGCGA TCCCGTGCAG AGCTTGGCGT AATCATGGTC ATAGCTGTT CCTGTGTGAA 7080
 7037 8
 PUC 19
 ATTGTTATCC GCTCACAAATT CCACACAAACA TACGAGGCCGG AAGCATAAAG TGTAAAGCCT 7140
 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 7200
 AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260
 GTTTGCCTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCCG TCGGTGTTTC 7320
 GGCTGCCGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTAATCC ACAGAACATCAG 7380
 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAUG AACCGTAAAA 7440
 7461=BACTERIAL ORIGIN OF REPLICATION
 AGGCCGCGTT GCTGGCGTT TCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC 7500

FIG. 3E

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GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAAG GCGTTCCCC 7560
 CTGGAAAGCTC CCTCGTGCAG TCTCCTGTT CGACCCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTGGGGAAGC GTGGCGCTT CTCATGCTC ACGCTGTAGG TATCTCAGTT 7680
 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTT GAGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTGAA GTGGTGGCCT AACTACGGCT ACACATAGAAG GACAGTATTG GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTGGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAAACAAA 7980
 CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAAGT 8100
 CACGTTAAGG GATTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTAA 8160
STOP
ATTAAGGAAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT 8220
BETA LACTAMASE
ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTCGT TCATCCATAG 8280
TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACCC 8400
BETA LACTAMASE=861bp=286 AMINO ACID & STOP CODON
AGCCAGCCGG AAGGGCCGAG CGCAGAAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG 8520
TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA 8580
GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
TTAGCTCCTT CGGTCCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA 8700
TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTCTG 8760
TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCCA CCGAGTTGCT 8820
CTTGGCCGGC GTCAATAACCG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
GGTCGATGTA ACCCAACTCGT GCACCCAACT GATCTTCAGC ATCTTTACT TTCACCAGCG 9000
TTTCTGGGTG AGCAAAACAA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
GGAAATGTTG AATACTCATC CTCTTCCCTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
ATTGTCTCAT GAGCGGATAC ATATTGAAT GTATTTAGAA AAATAAAACAA ATAGGGGTTC 9180
CGCGCACATT TCCCCGAAAA GTGCCACCT

FIG. 3F

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LEADER

FRAME 1	Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val	-20	-15	-10				
	ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC				S!			
	987 996 1005 1014 1023							
-5	Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser	10						
	ATA ATG TCC AGA GGA CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT							
	1038 1047 1056 1065 1074 1083							
20	Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Val Ser Tyr Ile His	23	CDR1	27/ 29	30	34		
	CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AGT TAC ATC CAC							
	1095 1104 1113 1122 1131 1140							
35	FR2	40	45	49	50	CDR2		
	Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn							
	TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC							
	1152 1161 1170 1179 1188 1197							
55	56	57	60	FR3	65	70		
	Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser							
	CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT							
	1209 1218 1227 1235 1245 1254							
75	80	85	88	89	90			
	Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp							
	CTC ACC ATC AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG							
	1266 1275 1284 1293 1302 1311							
CDR3	95	97	98	100	FR4	105	107	
	Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys							
	ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA							
	1323 1332 1341 1350 1359							

FIG. 4

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LEADER

-19	-15	-10	-5															
Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	Val		
ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	GTC		
2409		2418		2427		2436		2445										
-1 ⁵ ₁ FR1 10 15																		
Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys	^{WY} _{Ala}	Gly	Ala	Ser
CTG	TCC	CAG	GTA	CAA	CTG	CAG	CAG	CCT	GGG	GCT	GAG	CTG	GTG	AAG	^{WY} _{CCT}	GGG	GCC	TCA
2460		2469		2478		2487		2496		2505								
20 25 30 31 CDR1 35 36																		
Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Asn	Met	His	Trp
GTG	AAG	ATG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACA	TTT	ACC	AGT	TAC	AAT	ATG	CAC	TGG
2517		2526		2536		2544							2553		2562			
40 FR2 45 49 50 52 52A 53 54																		
Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn
GTA	AAA	CAG	ACA	CCT	GGT	CGG	GGC	CTG	GAA	TGG	ATT	GGA	GCT	ATT	TAT	CCC	EEA	AAT
2574		2583		2592		2601							2610		2619			
55 CDR2 60 65 66 FR3 70																		
Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys
GGT	GAT	ACT	TCC	TAC	AAT	CAG	AAG	TTC	AAA	GGC	AAG	GCC	ACA	TTG	ACT	GCA	GAC	AAA
2631		2640		2649		2658							2667		2676			
75 80 82 82A 82B 82C 83 85																		
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
TCC	TCC	AGC	ACA	GCC	TAC	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	TCT	GCG	GTC	
2688		2697		2706		2715							2724		2733			
90 94 95 CDR3 100 100A 100B 100C 100D 101 102 103																		
Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn	Val	Trp	Gly
TAT	TAC	TGT	GCA	AGA	TCG	ACT	TAC	TAC	GGC	GGT	GAC	TGG	TAC	TTC	AAT	GTC	TGG	GGC
2745		2754		2763		2772							2781		2790			
105 FR4 110 113																		
Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala										
GCA	GGG	ACC	ACG	GTC	ACC	GTC	TCT	GCA										
2802		2811		2820														

FIG. 5

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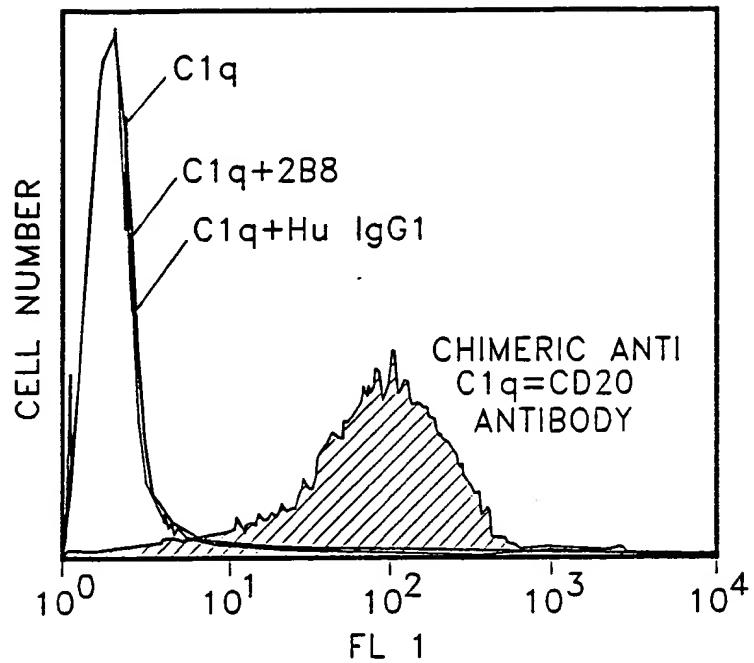


FIG. 6

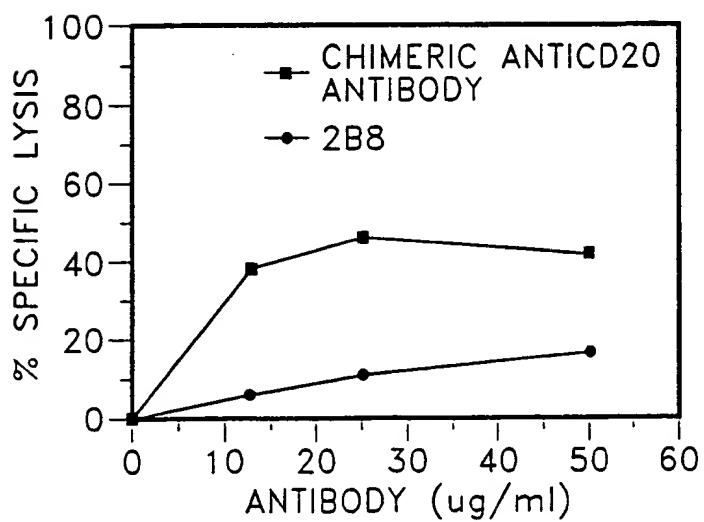


FIG. 7

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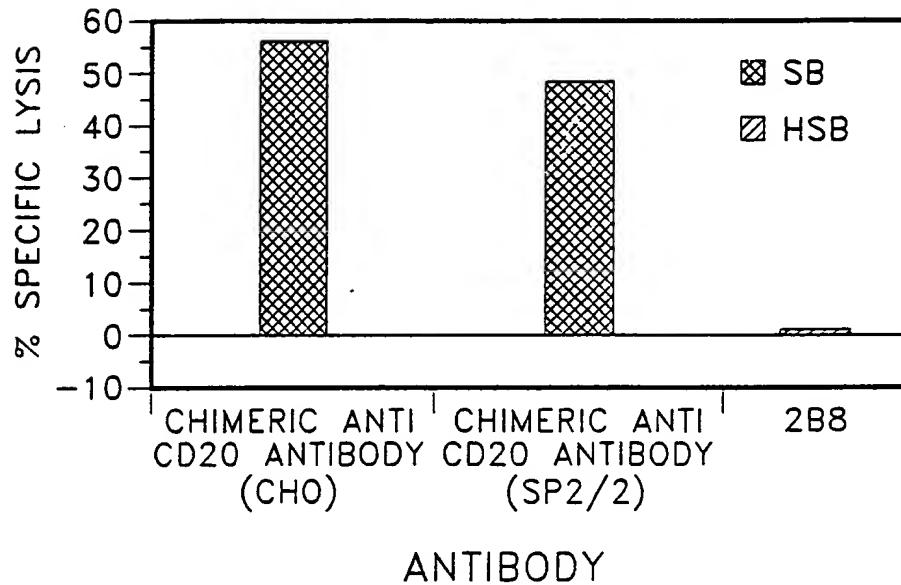


FIG. 8

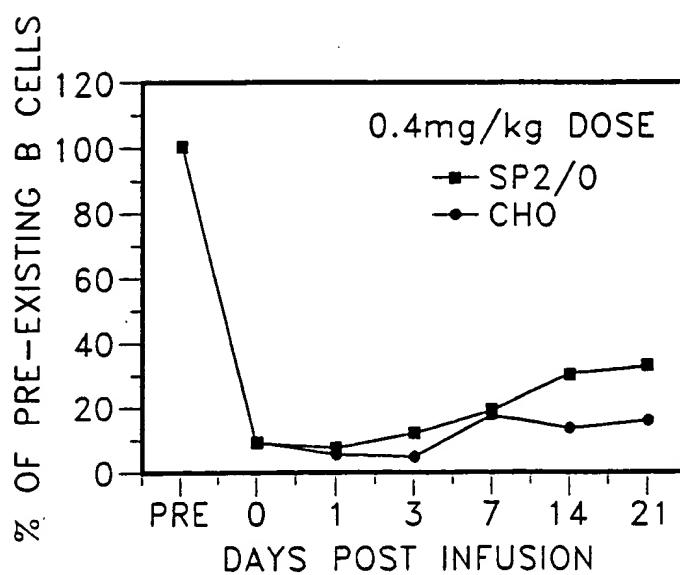


FIG. 9A

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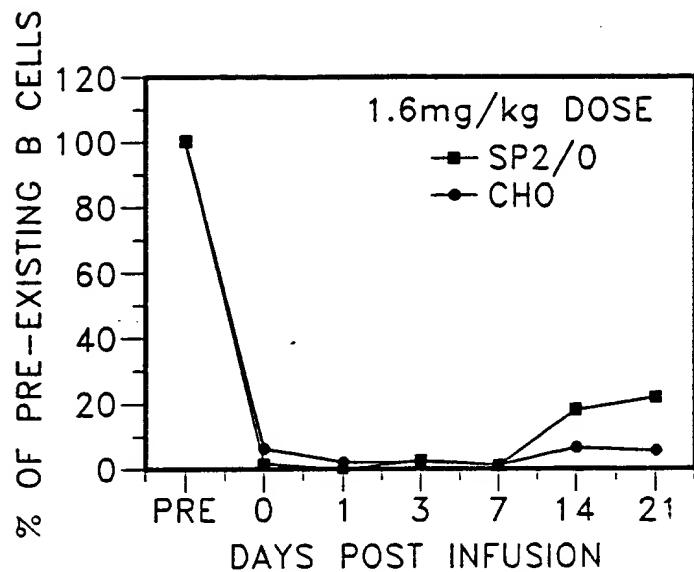


FIG. 9B

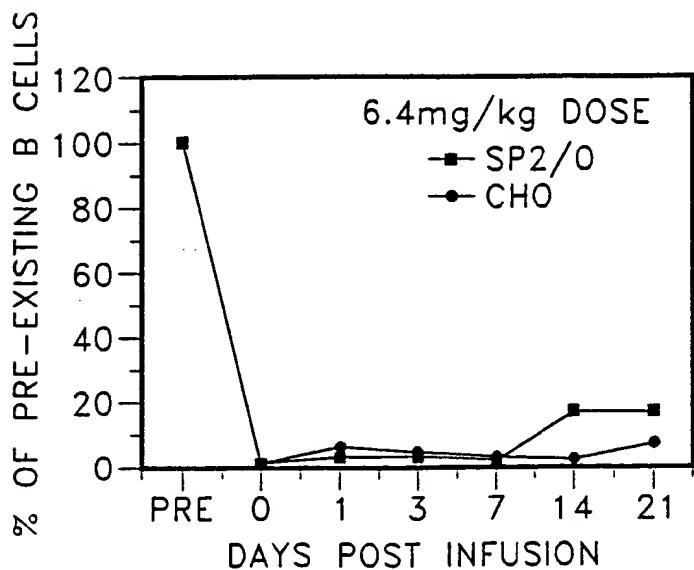


FIG. 9C

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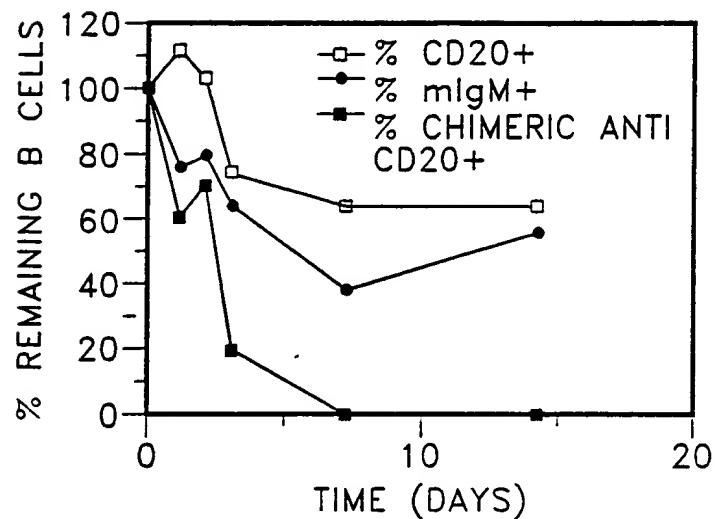


FIG. 10

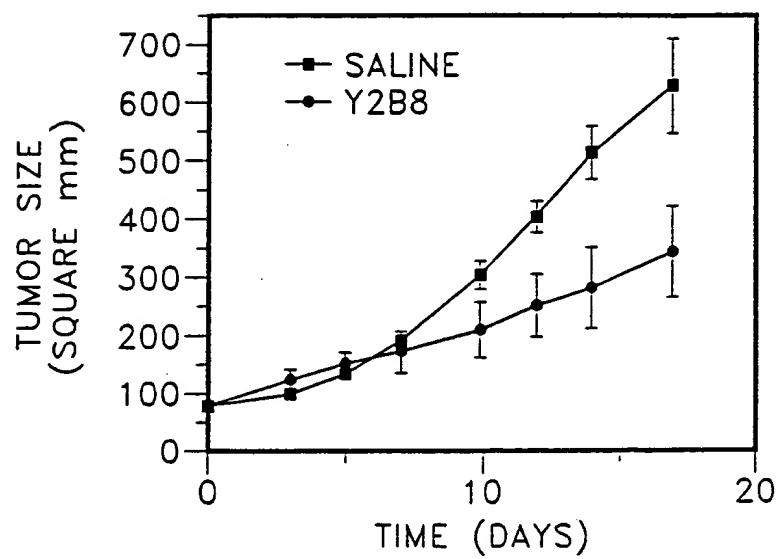


FIG. 11

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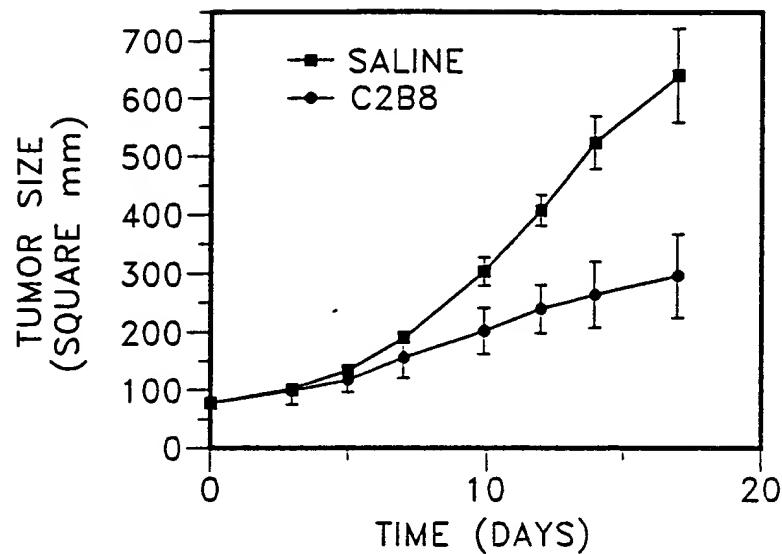


FIG. 12

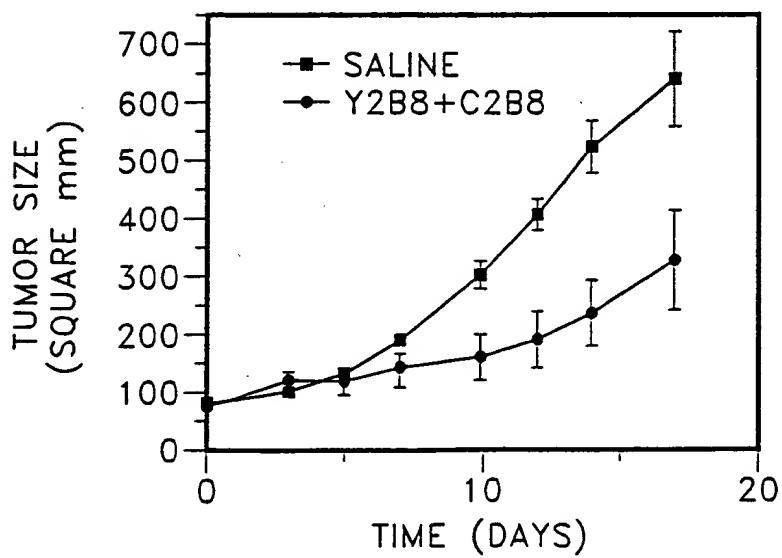
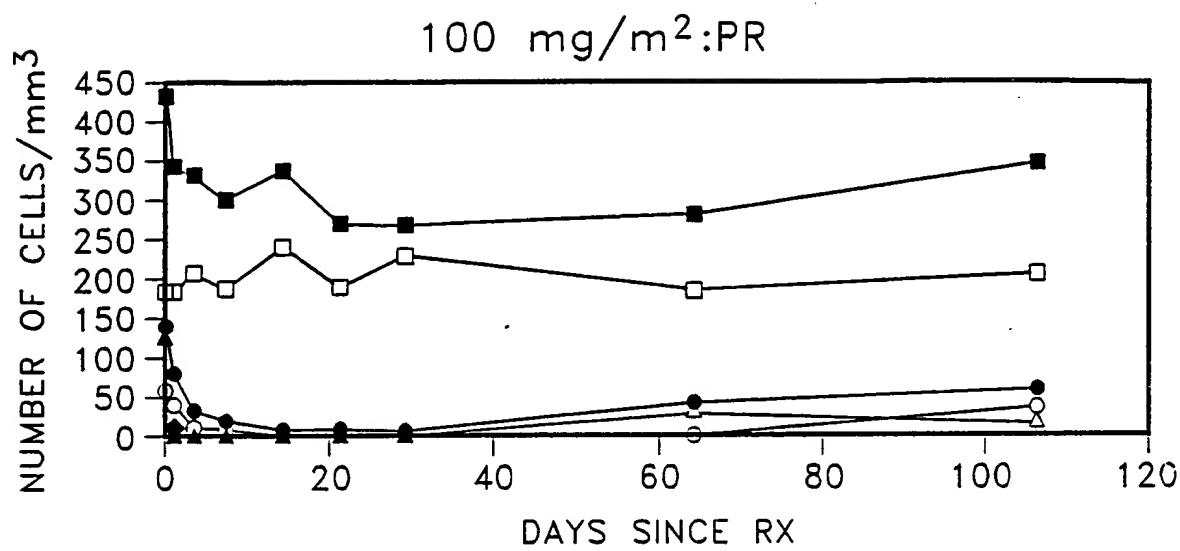


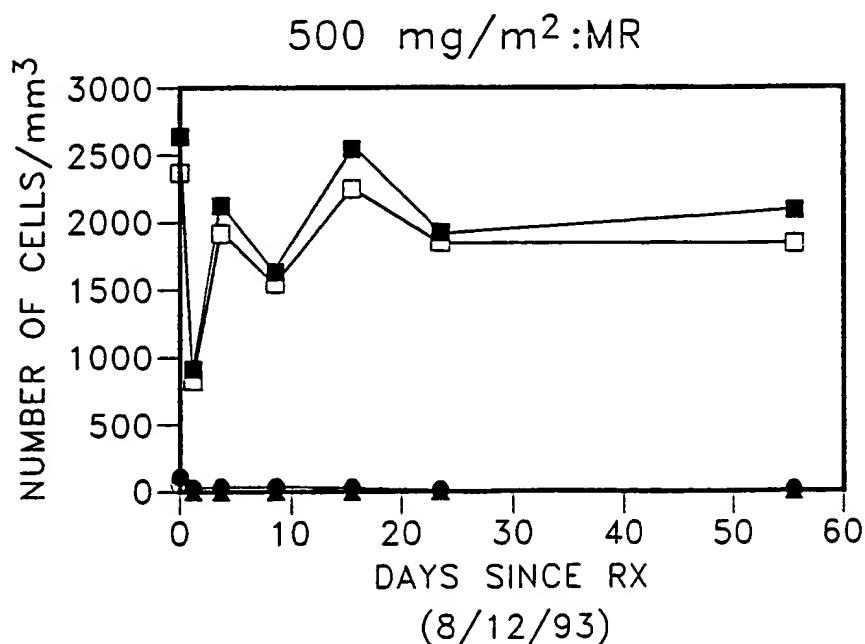
FIG. 13

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(8/12/93)
03 HEGMAJ
FIG. 14A



(8/12/93)

FIG. 14B

Figure 1
Binding of IDEC-C2B8 to CDW32 Mouse Fibroblast Cells Transfected with
Human Low Affinity Fc γ RII Membrane Receptors

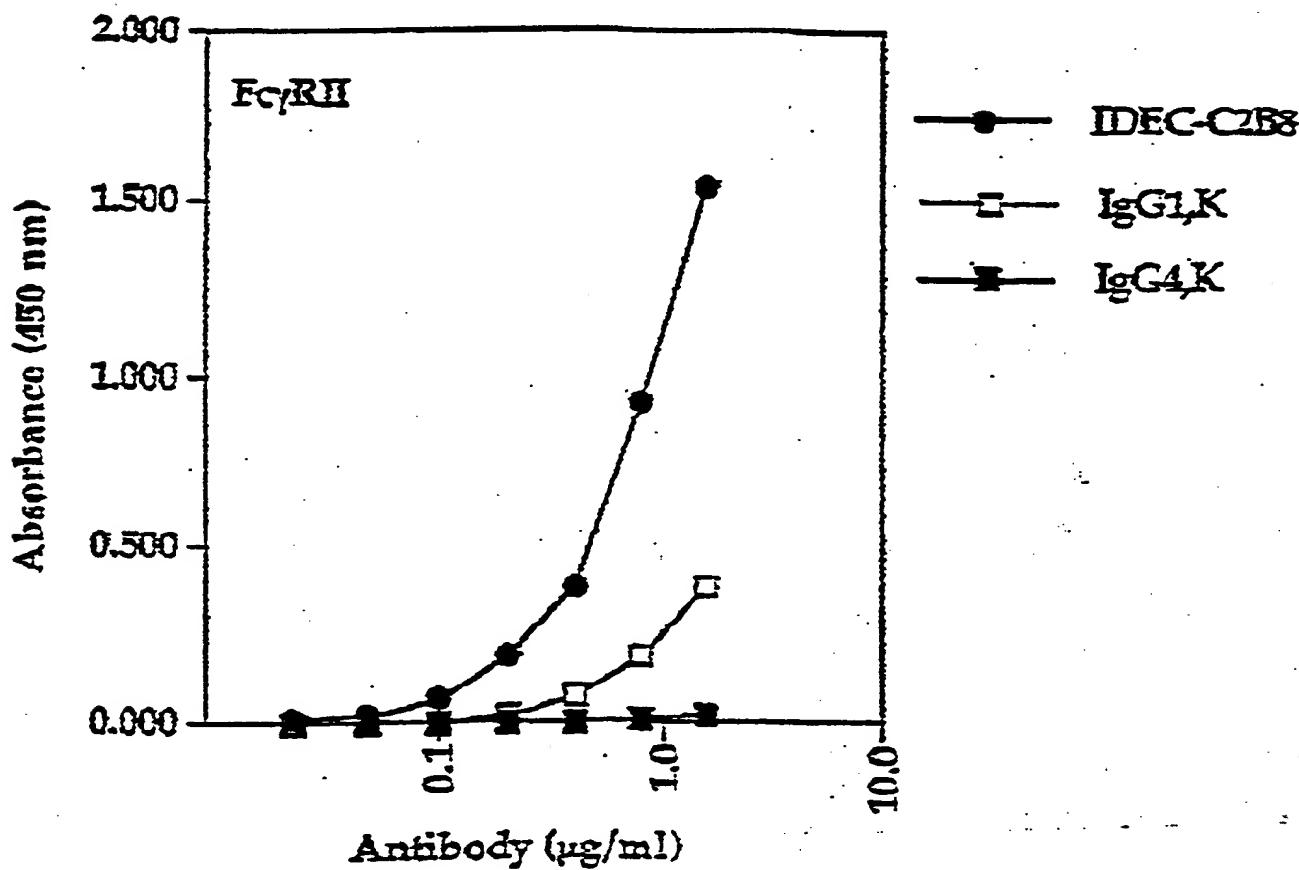


Figure 1. IDEC-C2B8 antibody was serially diluted in the absence of CD20, along with positive and negative isotype control human IgG1 and IgG4 antibodies. Aliquots were added in triplicate to sets of wells each containing Fc γ RII (human type II Fc receptor) transfected CDW32 mouse L cells. Binding of antibodies to Fc receptors was determined by ELISA. These results indicate that IDEC-C2B8 binds much more strongly to the low affinity human Fc γ RII receptor than typical human IgG1 antibodies with similar receptor binding sites.